

SCORE Search Results Details for Application 10516759 and Search Result 20081112_112527_us-10-516-759-14_copy_24_81.rpr.

| | | | | |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
| Score Home | Retrieve Application | SCORE System | SCORE | Comments / |
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This page gives you Search Results detail for the Application 10516759 and Search Result 20081112_112527_us-10-516-759-14_copy_24_81.rpr.

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GenCore version 6.3
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OM protein - protein search, using sw model

Run on: November 12, 2008, 12:14:54 ; Search time 9 Seconds
(without alignments)
620.064 Million cell updates/sec

Title: US-10-516-759-14_COPY_24_81
Perfect score: 350
Sequence: 1 DIKHNPRRDCVAEGKVCDP.....RNYSGGVCVTHCNFLNGEP 58

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|------------|-------|---------|--------|----|--------|--------------------|
| | | Match | Length | | | |
| 1 | 350 | 100.0 | 1342 | 2 | A36223 | kinase-related tra |
| 2 | 298 | 85.1 | 1339 | 2 | JC4387 | epidermal growth f |

| | | | | | | |
|----|-------|------|------|---|--------|--------------------|
| 3 | 212 | 60.6 | 1308 | 2 | A47253 | epidermal growth f |
| 4 | 201 | 57.4 | 644 | 2 | A36325 | epidermal growth f |
| 5 | 200 | 57.1 | 1210 | 2 | A53183 | epidermal growth f |
| 6 | 198 | 56.6 | 1223 | 1 | TVCHLV | epidermal growth f |
| 7 | 179 | 51.1 | 1210 | 1 | GQHUE | epidermal growth f |
| 8 | 174 | 49.7 | 1255 | 1 | A24571 | protein-tyrosine k |
| 9 | 166.5 | 47.6 | 1260 | 1 | TVRTNU | protein-tyrosine k |
| 10 | 150.5 | 43.0 | 1369 | 2 | S70713 | protein-tyrosine k |
| 11 | 143.5 | 41.0 | 1166 | 1 | S06142 | protein-tyrosine k |
| 12 | 142 | 40.6 | 1254 | 2 | I48161 | p-185 precursor - |
| 13 | 133 | 38.0 | 843 | 2 | A27131 | epidermal growth f |
| 14 | 128.5 | 36.7 | 1323 | 2 | E88257 | protein let-23 [im |
| 15 | 128.5 | 36.7 | 1374 | 2 | S70712 | protein-tyrosine k |
| 16 | 115 | 32.9 | 1299 | 2 | T43251 | furin (EC 3.4.21.7 |
| 17 | 107 | 30.6 | 1680 | 2 | A43434 | furin (EC 3.4.21.7 |
| 18 | 97.5 | 27.9 | 915 | 2 | B48225 | probable proprotei |
| 19 | 96.5 | 27.6 | 915 | 1 | A48225 | subtilisin-like pr |
| 20 | 96.5 | 27.6 | 1548 | 2 | S34583 | serine proteinase |
| 21 | 95.5 | 27.3 | 899 | 2 | G02428 | subtilisin-like pr |
| 22 | 95.5 | 27.3 | 915 | 2 | JC6148 | subtilisin-like pr |
| 23 | 95.5 | 27.3 | 969 | 1 | A39490 | subtilisin-like pr |
| 24 | 95.5 | 27.3 | 975 | 2 | JC5570 | subtilisin-like pr |
| 25 | 93.5 | 26.7 | 962 | 2 | JC5571 | subtilisin-like pr |
| 26 | 90.5 | 25.9 | 631 | 2 | JC2345 | kexin-like protein |
| 27 | 90.5 | 25.9 | 644 | 2 | JC2346 | kexin-like protein |
| 28 | 90.5 | 25.9 | 932 | 2 | I52527 | PACE4A - mouse (fr |
| 29 | 90.5 | 25.9 | 937 | 2 | I53282 | gene PACE4 protein |
| 30 | 89 | 25.4 | 1717 | 1 | A45558 | epidermal growth f |
| 31 | 87 | 24.9 | 1372 | 2 | A34157 | insulin receptor p |
| 32 | 87 | 24.9 | 1383 | 2 | A36080 | insulin receptor p |
| 33 | 86 | 24.6 | 1382 | 1 | INHUR | insulin receptor p |
| 34 | 84 | 24.0 | 427 | 2 | T29872 | hypothetical prote |
| 35 | 84 | 24.0 | 1367 | 1 | IGHUR1 | insulin-like growt |
| 36 | 82 | 23.4 | 1330 | 1 | GQFFE | epidermal growth f |
| 37 | 82 | 23.4 | 1371 | 2 | A33837 | insulin-like growt |
| 38 | 77.5 | 22.1 | 2101 | 2 | S57245 | insulin receptor (|
| 39 | 77.5 | 22.1 | 2148 | 1 | A56081 | insulin receptor - |
| 40 | 77 | 22.0 | 1363 | 2 | T43220 | insulin-like growt |
| 41 | 74 | 21.1 | 1268 | 2 | B36502 | insulin receptor-r |
| 42 | 73.5 | 21.0 | 1607 | 2 | T43212 | insulin-like growt |
| 43 | 73 | 20.9 | 540 | 2 | B47417 | insulin receptor-r |
| 44 | 72 | 20.6 | 329 | 2 | A48805 | insulin-like growt |
| 45 | 71.5 | 20.4 | 1274 | 2 | T42017 | cysteine rich prot |

ALIGNMENTS

RESULT 1

A36223

kinase-related transforming protein (erbB3) (EC 2.7.1.-) precursor - human

C;Species: Homo sapiens (man)

C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 31-Dec-2004

C;Accession: A36223; I59164

R;Kraus, M.H.; Issing, W.; Miki, T.; Popescu, N.C.; Aaronson, S.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989

A;Title: Isolation and characterization of ERBB3, a third member of the ERBB/epidermal

http://es.ScoreAccessWeb/GetItem.action?AppId=105167...-10-516-759-14_copy_24_81.rpe&ItemType=4&startByte=0 (5 of 17)11/22/2008 11:35:38 AM

A;Title: Epidermal growth factor receptor threonine and serine residues phosphorylated in vivo.
A;Reference number: A28941; MUID:88330814; PMID:3138233
A;Accession: A28941
A;Molecule type: protein
A;Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995-996,'X',998-1000;1002-1009,'D',1011-1015,'X',1017-1025;1028-1033;1069-1070,'X',1072-1076,'L' <HEI>
A;Cross-references: UNIPARC:UPI0000175617; UNIPARC:UPI0000175618; UNIPARC:UPI0000175619; UNIPARC:UPI000017561A; UNIPARC:UPI000017561B
R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
submitted to the EMBL Data Library, April 1994
A;Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor and comparison to its human homologue.
A;Reference number: S45325
A;Accession: S45325
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-971,'K',973-1210 <VER>
A;Cross-references: UNIPARC:UPI000002182B; EMBL:X78987; NID:g488830; PIDN:CAA55587.1; PID:g488831
R;Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993
A;Title: Expression of the epidermal growth factor receptor gene is regulated in mouse blastocysts during delayed implantation.
A;Reference number: I49643; MUID:93126380; PMID:7678348
A;Accession: I49643
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 12-20,22-132 <RES>
A;Cross-references: UNIPARC:UPI000016CD26; GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201
C;Genetics:
A;Gene: EGFR
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;648-670/Domain: transmembrane #status predicted <TMM>
F;712-977/Domain: protein kinase homology <KIN>
F;720-728/Region: protein kinase ATP-binding motif
F;680,695/Binding site: phosphate (Thr) (covalent) #status experimental
F;697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental
F;993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental
F;1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
F;1197/Binding site: phosphate (Tyr) (covalent) #status experimental

Query Match 57.1%; Score 200; DB 2; Length 1210;
Best Local Similarity 59.6%; Pred. No. 2.1e-12;
Matches 34; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

Qy 2 IKHNRPRRDCAEGKVCDCPLCSSGGCGWPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
| :| :|| | ||:|||| | ||| | |:|:| || | | | |||
Db 490 IMNNRAEKDKCAVNHVCNPLCSSEGCWGPEPRDCVSCQNVSRGECVEKCNILEGEP 546

RESULT 6
TVCHLV

epidermal growth factor receptor precursor - chicken
 N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
 C;Species: Gallus gallus (chicken)
 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 05-Oct-2004
 C;Accession: A27720; A00643
 R;Lax, I.; Johnson, A.; Howk, R.; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Vennstrom, B.; Schlessinger, J.; Givol, D.
 Mol. Cell. Biol. 8, 1970-1978, 1988
 A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in mouse cells, and differential binding of EGF and transforming growth factor alpha.
 A;Reference number: A27720; MUID:88261272; PMID:3260329
 A;Accession: A27720
 A;Molecule type: mRNA
 A;Residues: 1-1223 <LAX>
 A;Cross-references: UNIPROT:P00534; UNIPARC:UPI00001725C3; GB:M20386
 R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M. A.; Kung, H.J.
 Cell 41, 719-726, 1985
 A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and promoter insertion result in expression of an amino-truncated EGF receptor.
 A;Reference number: A00643; MUID:85228222; PMID:2988784
 A;Accession: A00643
 A;Molecule type: mRNA
 A;Residues: 585-1223 <NIL>
 A;Cross-references: UNIPARC:UPI00001725C4; GB:M10066
 C;Genetics:
 A;Gene: erbB
 C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
 C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor receptor; oncogene; phosphoprotein; phosphotransferase; transforming protein; transmembrane protein; tyrosine-specific protein kinase
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-1223/Product: epidermal growth factor receptor #status predicted <MAT>
 F;31-654/Domain: extracellular #status predicted <EXT>
 F;81-307/Domain: EGF receptor extracellular domain repeat <EE1>
 F;397-610/Domain: EGF receptor extracellular domain repeat <EE2>
 F;655-677/Domain: transmembrane #status predicted <TMM>
 F;678-1223/Domain: intracellular #status predicted <INT>
 F;719-984/Domain: protein kinase homology <KIN>
 F;727-735/Region: protein kinase ATP-binding motif
 F;136,202,280,361,370,422,575,580,615,635/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F;192,650/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;687/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F;754/Active site: Lys #status predicted
 F;1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 56.6%; Score 198; DB 1; Length 1223;
 Best Local Similarity 59.6%; Pred. No. 3.3e-12;
 Matches 34; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

Qy 2 IKHNRPRRDCAEGKVCDPLCSSGGCWGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 | | : | | : | | | | | | | | | | : | | | | |
 Db 497 IIQNRNKNDCTADRHVCDPLCSDVGCWGPFGFHCFSRFFSRQKECVKQCINILQGEF 553

RESULT 7

GQHUE

epidermal growth factor receptor precursor - human

N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB

C;Species: Homo sapiens (man)

C;Date: 15-Nov-1984 #sequence_revision 27-Nov-1985 #text_change 05-Oct-2004

C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; A60143; A33331

R;Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, J.;

Yarden, Y.; Libermann, T.A.; Schlessinger, J.; Downward, J.; Mayes, E.L.V.; Whittle, N.;

Waterfield, M.D.; Seeburg, P.H.

Nature 309, 418-425, 1984

A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cells.

A;Reference number: A00641; MUID:84219729; PMID:6328312

A;Accession: A00641

A;Molecule type: mRNA

A;Residues: 1-1210 <ULL>

A;Cross-references: UNIPROT:P00533; UNIPARC:UPI0000050F30; EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924

A;Note: the authors translated the codon AAG for residue 540 as Asn

R;Tshii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.

Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985

A;Title: Characterization and sequence of the promoter region of the human epidermal growth factor receptor gene.

A;Reference number: A25772; MUID:85270438; PMID:2991899

A;Accession: A25772

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-29 <ISH>

A;Cross-references: UNIPARC:UPI000016A882; GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272

R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.

Oncogene Res. 1, 375-396, 1987

A;Title: The human EGF receptor gene: structure of the 110 kb locus and identification of sequences regulating its transcription.

A;Reference number: S30024; MUID:88217333; PMID:3329716

A;Accession: S30024

A;Molecule type: DNA

A;Residues: 1-29 <HA2>

A;Cross-references: UNIPARC:UPI000016A882; EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119

R;Haley, J.D.; Waterfield, M.D.

J. Biol. Chem. 266, 1746-1753, 1991

A;Title: Contributory effects of de Novo transcription and premature transcript termination in the regulation of human epidermal growth factor receptor proto-oncogene RNA synthesis.

A;Reference number: A38672; MUID:91107677; PMID:1988448

A;Accession: A38672

A;Molecule type: DNA

A;Residues: 1-29 <HAL>

A;Cross-references: UNIPARC:UPI000016A882; GB:M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271

A;Experimental source: carcinoma cell line A431-7

R;Xu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.;

Merlino, G.T.; Pastan, I.

Nature 309, 806-810, 1984

A;Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs overproduced in A431 carcinoma cells.

A;Reference number: A00642; MUID:84245835; PMID:6330563
A;Accession: A00642
A;Molecule type: mRNA
A;Residues: 'RCAWRR',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-321,'A',323-372,374-502,504,'GSAMP',510,'A',512,'R',514-517,'RA',521-539,'N',541-667,'IG',670-676,'A',678-794,'SAG',798-799,'TD',802-811,'R',813-942 <XUY>
A;Cross-references: UNIPARC:UPI00001725BD
A;Experimental source: A431 human carcinoma cells, which have large numbers of EGF receptors (a 30-fold amplification of DNA sequence and possible rearrangements) and elevated EGF-binding capacity
R;Lin, C.R.; Chen, W.S.; Krueger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.M.; Gill, G.N.; Rosenfeld, M.G.
Science 224, 843-848, 1984
A;Title: Expression cloning of human EGF receptor complementary DNA: gene amplification and three related messenger RNA products in A431 cells.
A;Reference number: A43615; MUID:84196372; PMID:6326261
A;Accession: A43615
A;Molecule type: mRNA
A;Residues: 713-964 <LIN>
A;Cross-references: UNIPARC:UPI00001725BE
A;Experimental source: epidermoid carcinoma cell line A431
R;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley, B.W.
Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A;Reference number: A23062; MUID:85046483; PMID:6093780
A;Accession: A23062
A;Molecule type: mRNA
A;Residues: 1028-1210 <SIM>
A;Cross-references: UNIPARC:UPI00001725BF
R;Weber, W.; Gill, G.N.; Spiess, J.
Science 224, 294-297, 1984
A;Reference number: A05281; MUID:84172183; PMID:6324343
A;Accession: A05281
A;Molecule type: protein
A;Residues: 25-30,'S',32-51;454-467 <WEB>
A;Cross-references: UNIPARC:UPI00001725C0; UNIPARC:UPI00001725C1
R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 5205-5208, 1985
A;Title: Identification of residues in the nucleotide binding site of the epidermal growth factor receptor/kinase.
A;Reference number: A60143; MUID:85182650; PMID:2985580
A;Accession: A60143
A;Molecule type: protein
A;Residues: 740-744,'X',746-747 <RUS>
A;Cross-references: UNIPARC:UPI00001725C2
R;Mroczkowski, B.; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
A;Title: ATP-stimulated interaction between epidermal growth factor receptor and supercoiled DNA.
A;Reference number: A38023; MUID:84191554; PMID:6325948
A;Contents: annotation; receptor activity
A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA
R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J.; Wiley, H.S.; Gill, G.N.; Rosenfeld, M.G.
Cell 59, 33-43, 1989
A;Title: Functional independence of the epidermal growth factor receptor from a domain required for ligand-induced internalization and calcium regulation.
A;Reference number: A33331; MUID:90003233; PMID:2790960

A;Contents: annotation; internalization signal
 C;Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation of cell DNA synthesis, and cell proliferation.
 C;Genetics:
 A;Gene: GDB:EGFR
 A;Cross-references: GDB:120610; OMIM:131550
 A;Map position: 7p12.3-7p12.1
 C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
 C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphotransferase; proto-oncogene; receptor; transmembrane protein; tyrosine-specific protein kinase
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-1210/Product: EGF receptor #status predicted <MAT>
 F;25-645/Domain: extracellular #status predicted <EXT>
 F;75-300/Domain: EGF receptor extracellular domain repeat <EE1>
 F;390-600/Domain: EGF receptor extracellular domain repeat <EE2>
 F;646-668/Domain: transmembrane #status predicted <TMM>
 F;669-1210/Domain: intracellular #status predicted <INT>
 F;710-975/Domain: protein kinase homology <KIN>
 F;718-726/Region: protein kinase ATP-binding motif
 F;999-1046/Region: coated-pit mediated internalization signal
 F;1047-1210/Region: inhibitory
 F;128,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;745/Active site: Lys #status experimental

Query Match 51.1%; Score 179; DB 1; Length 1210;
 Best Local Similarity 57.4%; Pred. No. 2.6e-10;
 Matches 31; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 5 | NRPRRDCAEAGKVCDDPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP | 58 |
| | | : : | |
| Db | 493 | NRGENSKCATGQVCHALCSPGCGWPEPRDCVSCRNVSRGRECVDKCKLLEGE | 546 |

RESULT 8

A24571
 protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human
 N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB2;
 v-erbB-related protein HER-2/neu
 C;Species: Homo sapiens (man)
 C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 05-Oct-2004
 C;Accession: A24571; A25491; A44188; B44188; I59509; I57622
 R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.; Toyoshima, K.
 Nature 319, 230-234, 1986
 A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth factor receptor.
 A;Reference number: A24571; MUID:86118663; PMID:3003577
 A;Accession: A24571
 A;Molecule type: mRNA
 A;Residues: 1-1255 <YAM>
 A;Cross-references: UNIPROT:P04626; UNIPARC:UPI000003F55F; GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
 R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
 Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
 A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermal

growth factor-receptor gene and is amplified in a human salivary adenocarcinoma.
A;Reference number: A25491; MUID:86016729; PMID:2995967
A;Accession: A25491
A;Molecule type: DNA
A;Residues: 737-1031 <SEM>
A;Cross-references: UNIPARC:UPI000016A8A7; GB:M11767; NID:g182163; PIDN:AAA35808.1; PID: g553282
R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P. H.; Libermann, T.A.; Schlessinger, J.; Francke, U.; Levinson, A.; Ullrich, A.
Science 230, 1132-1139, 1985
A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromosomal location with neu oncogene.
A;Reference number: A44188; MUID:86070181; PMID:2999974
A;Accession: A44188
A;Molecule type: DNA
A;Residues: 740-910 <COU1>
A;Cross-references: UNIPARC:UPI000016AA26; GB:M12036; NID:g183988; PIDN:AAA35978.1; PID: g183989
A;Accession: B44188
A;Molecule type: mRNA
A;Residues: 1-517, 'RALL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <COU2>
A;Cross-references: UNIPARC:UPI00001725C7; GB:M11730; NID:g183986
R;King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A;Reference number: I59509; MUID:85272597; PMID:2992089
A;Accession: I59509
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 832-909 <REX>
A;Cross-references: UNIPARC:UPI0000070A3F; GB:L29395; NID:g459807; PIDN:AAA35809.1; PID: g459808
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional initiation.
A;Reference number: I57622; MUID:87286898; PMID:3039351
A;Accession: I57622
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-191 <TAL>
A;Cross-references: UNIPARC:UPI0000000427; GB:M16792; NID:g183983; PIDN:AAA58637.1; PID: g553332
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 30% of human breast and ovarian cancers.
C;Genetics:
A;Gene: GDB:ERBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120613; OMIM:164870
A;Map position: 17q21.1-17q21.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphotransferase; proto-oncogene; receptor; transforming protein; transmembrane protein; tyrosine-specific protein kinase

F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
 F;22-653/Domain: extracellular #status predicted <EXT>
 F;70-304/Domain: EGF receptor extracellular domain repeat <EE1>
 F;395-605/Domain: EGF receptor extracellular domain repeat <EE2>
 F;654-675/Domain: transmembrane #status predicted <TMM>
 F;676-1255/Domain: intracellular #status predicted <INT>
 F;718-983/Domain: protein kinase homology <KIN>
 F;726-734/Region: protein kinase ATP-binding motif
 F;68,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F;753/Active site: Lys #status predicted
 F;1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
 #status predicted

Query Match 49.7%; Score 174; DB 1; Length 1255;
 Best Local Similarity 51.9%; Pred. No. 8.2e-10;
 Matches 28; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 5 NRPRRDCV AEGKVC DPLC SSGGCW GPGQCL SCRNYS RGGVCV THCNFLNGEP 58
 ||| :|| | | ||: | ||||| |||:: | : || | | | |
 Db 498 NRPEDCV GEG LACHQL CARGHCW GPGPTQ CVNC S QFLRGQCEV EBCRV LQGLP 551

RESULT 9

TVRTINU

protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004

C;Accession: A24562; A61204

R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.

Nature 319, 226-230, 1986

A;Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.

A;Reference number: A24562; MUID:86118662; PMID:3945311

A;Accession: A24562

A;Molecule type: mRNA

A;Residues: 1-1260 <BAR>

A;Cross-references: UNIPROT:P06494; UNIPARC:UPI0000161B83; EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746

R;Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen, S.M. Carcinogenesis 12, 1975-1978, 1991

A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no mutation in urinary bladder carcinomas induced by N-butyl-N-(4-hydroxybutyl)nitrosamine, N-[4-(5-nitro-2-furyl)-2-thiazolyl]formamide or N-methyl-N-nitrosourea.

A;Reference number: A61204; MUID:92035293; PMID:1682063

A;Accession: A61204

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 637-663, 'V', 665-702 <MAS>

A;Cross-references: UNIPARC:UPI00001725C8

A;Note: authors translated the codon GCA for residue 25 as Val

C;Genetics:

A;Gene: neu

C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology

C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphotransferase; proto-oncogene; transforming protein; transmembrane protein; tyrosine-specific protein kinase

F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
 F;658-680/Domain: transmembrane #status predicted <TMN>
 F;723-988/Domain: protein kinase homology <KIN>
 F;731-739/Region: protein kinase ATP-binding motif
 F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;691/Binding site: phosphate (Thr) (covalent) #status predicted
 F;758/Active site: Lys #status predicted
 F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 47.6%; Score 166.5; DB 1; Length 1260;
 Best Local Similarity 50.9%; Pred. No. 4.6e-09;
 Matches 28; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

Qy 5 NRPRRD-CVAEGKVCPLCSSGGCGWPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
 ||| | ||: | ||: ||: | ||||| ||::| :: || || | ||
 Db 502 NRPEEDLCVSSGLVCNSLCAHGHCWGPPTQCVNCSHFLRGQECVEECRVWKGLEP 556

RESULT 10

S70713
 protein-tyrosine kinase let-23 precursor homolog - *Caenorhabditis vulgaris*
 N;Alternate names: receptor tyrosine kinase let-23 homolog
 C;Species: *Caenorhabditis vulgaris*
 C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004
 C;Accession: S70713
 R;Sakai, T.; Koga, M.; Ohshima, Y.
 J. Mol. Biol. 256, 548-555, 1996
 A;Title: Genomic structure and 5' regulatory regions of the let-23 gene in the nematode *C. elegans*.
 A;Reference number: S70712; MUID:96177760; PMID:8604137
 A;Accession: S70713
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-1369 <SAK>
 A;Cross-references: UNIPROT:Q23821; UNIPARC:UPI000017A3EC; EMBL:D63427
 C;Genetics:
 A;Gene: let-23
 A;Introns: 42/1; 49/1; 83/1; 105/3; 155/3; 207/1; 280/1; 369/1; 408/1; 438/2; 555/1; 598/2;
 673/2; 733/3; 830/3; 882/3; 1147/1; 1247/3; 1274/1; 1309/1
 C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kinase
 F;1-28/Domain: signal sequence #status predicted <SIG>
 F;29-1369/Product: protein-tyrosine kinase let-23 homolog #status predicted <MAT>
 F;929-1194/Domain: protein kinase homology <KIN>
 F;937-945/Region: protein kinase ATP-binding motif

Query Match 43.0%; Score 150.5; DB 2; Length 1369;
 Best Local Similarity 40.7%; Pred. No. 1.9e-07;
 Matches 24; Conservative 12; Mismatches 20; Indels 3; Gaps 1;

Qy 2 IKHNRPRRD-CVAEGKVCPLCSSGGCGWPGPGQCLSCRNYSRGGVCVTHCN---FLNGE 57
 :: || |: |: |::|| |:| |||| | | || :: | ||: |: || :
 Db 546 VEENRDRKLCIEEEICDPNCNSRGCGWGRPEDCRECRTWNNMGTCVSKCDTIGFLRNQ 604

RESULT 11

S06142

protein-tyrosine kinase (EC 2.7.1.112) mrk-Y precursor - southern platyfish
 N;Alternate names: epidermal growth factor receptor homolog; kinase-related transforming protein Tu; melanoma-inducing protein
 C;Species: Xiphophorus maculatus (southern platyfish)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
 C;Accession: S06142; S13809
 R;Wittbrodt, J.; Adam, D.; Malitschek, B.; Maeueller, W.; Raulf, F.; Telling, A.; Robertson, S.M.; Scharl, M.
 Nature 341, 415-421, 1989
 A;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-inducing Tu locus in Xiphophorus.
 A;Reference number: S06142; MUID:90015140; PMID:2797166
 A;Accession: S06142
 A;Molecule type: DNA
 A;Residues: 1-1166 <WIT>
 A;Cross-references: UNIPROT:P13388; UNIPARC:UPI00001725C5; EMBL:X16891; NID:g65290; PIDN:CAA34770.1; PID:g65291
 R;Adam, D.; Maeueller, W.; Scharl, M.
 Oncogene 6, 73-80, 1991
 A;Title: Transcriptional activation of the melanoma inducing Xmrk oncogene in Xiphophorus.
 A;Reference number: S13807; MUID:91125882; PMID:1846957
 A;Accession: S13809
 A;Status: preliminary; translation not shown
 A;Molecule type: DNA
 A;Residues: 821-1025,'N',1027-1098,'A',1100-1166 <ADA>
 A;Cross-references: UNIPARC:UPI00001715E2; EMBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285
 C;Genetics:
 A;Gene: mrk
 A;Map position: Y
 A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
 C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
 C;Keywords: ATP; growth factor receptor; phosphotransferase; transmembrane protein; tyrosine-specific protein kinase
 F;1-25/Domain: signal sequence #status predicted <SIG>
 F;26-1166/Product: kinase-related transforming protein (Tu) #status predicted <MAT>
 F;707-972/Domain: protein kinase homology <KIN>
 F;715-723/Region: protein kinase ATP-binding motif

| | | | | |
|-----------------------|--------|--------------------|-------|----------------------------------|
| Query Match | 41.0%; | Score 143.5; | DB 1; | Length 1166; |
| Best Local Similarity | 51.0%; | Pred. No. 8.3e-07; | | |
| Matches | 25; | Conservative | 4; | Mismatches 19; Indels 1; Gaps 1; |

| | | | |
|----|-----|---|-----|
| Qy | 10 | DCVAEGKVCPLCCSSGGCGWPGGQCLSCRNYSRGGVCVTHCNFLNGEP | 58 |
| | | : : : : | |
| Db | 496 | DARTENQTCNNECEDGCGW-PGPTMCVSCLVHVRGGRCVASCNLLQGEF | 543 |

RESULT 12
 I48161
 p-185 precursor - golden hamster
 C;Species: Mesocricetus auratus (golden hamster)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
 C;Accession: I48161
 R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishikawa, T.
 Gene 140, 251-255, 1994
 A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.

A;Reference number: I48161; MUID:94193007; PMID:7908275
 A;Accession: I48161
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-1254 <RES>
 A;Cross-references: UNIPROT:Q60553; UNIPARC:UPI000012A111; GB:D16295; NID:g493236; PIDN: BAA03801.1; PID:g747595
 C;Genetics:
 A;Gene: neu
 C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
 C;Keywords: ATP
 F;718-983/Domain: protein kinase homology <KIN>
 F;726-734/Region: protein kinase ATP-binding motif

Query Match 40.6%; Score 142; DB 2; Length 1254;
 Best Local Similarity 42.6%; Pred. No. 1.2e-06;
 Matches 23; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

Qy 5 NRPRRDCAVEGKVCDDLPCSSGGCWGPGGQCLSCRNYSRGGVCTHNCNLFNGEP 58
 | : | : | ||| | |||| | ||: | : | | | |
 Db 498 NPSEEECKGLKDFACYPLCAHGHCWGPGPTQCVNCSHFLRGQECVKECRVWKGFL 551

RESULT 13

A27131

epidermal growth factor receptor - fruit fly (*Drosophila melanogaster*) (fragment)C;Species: *Drosophila melanogaster*

C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 31-Dec-2004

C;Accession: A27131

R;Schejter, E.D.; Segal, D.; Glazer, L.; Shilo, B.Z.

Cell 46, 1091-1101, 1986

A;Title: Alternative 5' exons and tissue-specific expression of the *Drosophila* EGF receptor homolog transcripts.

A;Reference number: A27131; MUID:87002474; PMID:3093080

A;Accession: A27131

A;Molecule type: mRNA

A;Residues: 1-843 <SCH>

A;Cross-references: UNIPROT:Q8MLW0; UNIPARC:UPI0000175612

C;Genetics:

A;Gene: FlyBase:Egfr

A;Cross-references: FlyBase:FBgn0003731

C;Superfamily: protein kinase homology

C;Keywords: ATP; growth factor receptor

Query Match 38.0%; Score 133; DB 2; Length 843;
 Best Local Similarity 37.8%; Pred. No. 7.3e-06;
 Matches 17; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Qy 11 CVAEGKVCDDLPCSSGGCWGPGGQCLSCRNYSRGGVCTHNCNLFN 55
 | | : | | : |||| | |||:|:| : | : :
 Db 517 CEKNGTICSDQCNEGDCWAGTIDQLCTCKNFNFGTICIADCGYIS 561

RESULT 14

E88257

protein let-23 [imported] - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004
 C;Accession: E88257
 R;anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology.
 A;Reference number: A75000; MUID:99069613; PMID:9851916
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/ for a list of authors
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 285, 1493, 1999
 A;Accession: E88257
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1323 <STO>
 A;Cross-references: UNIPARC:UPI0000164043; GB:chr_II; PIDN:CAA93882.1; PID:g3881523; GSPDB:GN00020
 C;Genetics:
 A;Gene: let-23
 A;Map position: 2

Query Match 36.7%; Score 128.5; DB 2; Length 1323;
 Best Local Similarity 39.0%; Pred. No. 2.8e-05;
 Matches 23; Conservative 7; Mismatches 26; Indels 3; Gaps 1;

Qy 2 IKHNRPRRDCAVAGKVCDDLCSGGCGWPGPGQCLSCRNYSGGVCTHNCN---FLNGE 57
 | | | : | | :|| | : ||| | || | : : | || | : || :
 Db 504 IAE NRDSKLCETEQRVCDDKNCNKRGCWKEPEDCLECKTWTWSVGTCEVKCDTKTGFLRNQ 562

RESULT 15

S70712
 protein-tyrosine kinase (EC 2.7.1.112) let-23 precursor - Caenorhabditis elegans
 N;Alternate names: receptor tyrosine kinase let-23
 C;Species: Caenorhabditis elegans
 C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004
 C;Accession: S70712; S73101; S13422; T27682
 R;Sakai, T.; Koga, M.; Ohshima, Y.
 J. Mol. Biol. 256, 548-555, 1996
 A;Title: Genomic structure and 5' regulatory regions of the let-23 gene in the nematode C. elegans.
 A;Reference number: S70712; MUID:96177760; PMID:8604137
 A;Accession: S70712
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-1374 <SAK>
 A;Cross-references: UNIPROT:P24348; UNIPARC:UPI000017A472; EMBL:D63426
 A;Experimental source: strain N2
 R;Koga, M.
 submitted to the EMBL Data Library, July 1995
 A;Reference number: S73101
 A;Accession: S73101
 A;Molecule type: DNA
 A;Residues: 1-50, 'G', 52-1374 <KOG>
 A;Cross-references: UNIPARC:UPI000016B8F7; EMBL:D63426; NID:g1407562; PIDN:BAA09729.1; PID:g1407563
 A;Experimental source: strain N2
 R;Aroian, R.V.; Koga, M.; Mendel, J.E.; Ohshima, Y.; Sternberg, P.W.

Nature 348, 693-699, 1990

A;Title: The let-23 gene necessary for *Caenorhabditis elegans* vulval induction encodes a tyrosine kinase of the EGF receptor subfamily.

A;Reference number: S13422; MUID:91080919; PMID:1979659

A;Accession: S13422

A;Molecule type: mRNA

A;Residues: 52-1374 <ARO>

A;Cross-references: UNIPARC:UPI0000164043

R;Thomas, K.

submitted to the EMBL Data Library, March 1996

A;Reference number: Z20404

A;Accession: T27682

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 52-1374 <WIL>

A;Cross-references: UNIPARC:UPI0000164043; EMBL:Z70038; PIDN:CAA93882.1; GSPDB:GN00020; CESP:ZK1067.1

A;Experimental source: clone ZK1067

C;Genetics:

A;Gene: let-23; CESP:ZK1067.1

A;Map position: 2

A;Introns: 44/1; 51/1; 90/1; 112/3; 165/3; 217/1; 290/1; 379/1; 418/1; 448/2; 565/1; 608/2; 682/2; 742/3; 836/3; 888/3; 1256/3; 1283/1; 1319/1

C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kinase

F;1-28/Domain: signal sequence #status predicted <SIG>

F;29-1374/Product: protein-tyrosine kinase let-23 #status predicted <MAT>

F;934-1199/Domain: protein kinase homology <KIN>

F;942-950/Region: protein kinase ATP-binding motif

Query Match 36.7%; Score 128.5; DB 2; Length 1374;
 Best Local Similarity 39.0%; Pred. No. 2.9e-05;
 Matches 23; Conservative 7; Mismatches 26; Indels 3; Gaps 1;

Qy 2 IKHNRPRRDCVAEGKVCDPLCSSGGCGWPGPGQCLSCRNYSRGGVCVTHCN---FLNGE 57
 | | | : | | :|| | : ||| | || | : | | | : | | :
 Db 555 IAENRDSKLCETEQRVCDKNCNKRGCWKEPEDCLECKTWNKSVGTCEVKCDTKGFLRNQ 613

Search completed: November 12, 2008, 12:15:04

Job time : 10 secs

SCORE 16